

Serial No. 09/981,289
Filed: October 15, 2001

Please amend the application as follows:

In the claims:

Please cancel claims 1-11 without prejudice or disclaimer as drawn to non-elected inventions.

Please add the following new claims:

- Sub 12/25/01
12. A method for generating a secondary library of scaffold protein variants comprising:
- a) generating a probability distribution table of amino acid residues in a plurality of variant positions utilizing a force field calculation; and
 - b) combining a plurality of said amino acid residues to generate a secondary library of secondary sequences;
- wherein at least one of said secondary variants is different from said primary variants.
13. A method according to claim 12, wherein said force field calculation is SCMF.
14. A method according to claim 12, further comprising computationally recombining said secondary library to generate a tertiary library.
15. A method according to claim 14, wherein Protein Design Automation (PDA™) is used to recombine said secondary library.
16. A method for generating a secondary library of scaffold protein variants comprising:
- a) generating a probability distribution table of amino acid residues in a plurality of variant positions utilizing an alignment program;
 - b) combining a plurality of said amino acid residues to generate a secondary library of secondary sequences, wherein at least one of said secondary variants is different from

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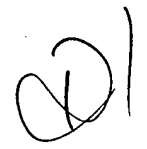
said primary variants; and

c) computational ranking said secondary library.

17. A method according to claim 16, further comprising computationally recombining said secondary library to generate a tertiary library.

18. A method according to claim 17, wherein PDATM is used to recombine said secondary library.

19. A method according to claim 16, wherein said alignment program is a sequence alignment program.

20. A method according to claim 16, wherein said alignment program is a structural alignment program.

21. A method according to claims 12 or 16 further comprising synthesizing a plurality of said secondary sequences.

22. A method according to claim 21 wherein said synthesizing is done by multiple PCR with pooled oligonucleotides.

23. A method according to 22 wherein said pooled oligonucleotides are added in equimolar amounts.